R.Hutson 10D4 (handwritten)

#9 (handwritten)

1652

RAW SEQUENCE LISTING   DATE: 02/14/2001
PATENT APPLICATION: US/09/269,860   TIME: 16:03:08

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  3 <110> APPLICANT: Ankenbauer, Waltraud
  4        Schmitz-Agheguian, Gudrun
  5        Elizaveta, Bonch-Osmolovskaya
  6        Svetlichny, Vitaly
  7        Ebenbichler, Christine
  8        Angerer, Bernhard
  9        Laue, Frank
 11 <120> TITLE OF INVENTION: Thermostable Nucleic Acid Polymerase From Thermococcus gorgonarius
 13 <130> FILE REFERENCE: 4453
 15 <140> CURRENT APPLICATION NUMBER: US 09/269,860
 16 <141> CURRENT FILING DATE: 2000-03-10
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP97/05393
 19 <151> PRIOR FILING DATE: 1997-10-01
 21 <150> PRIOR APPLICATION NUMBER: EP/97100584.8
 22 <151> PRIOR FILING DATE: 1997-01-16
 24 <150> PRIOR APPLICATION NUMBER: EP/96115874.8
 25 <151> PRIOR FILING DATE: 1996-10-03
 27 <160> NUMBER OF SEQ ID NOS: 9
 29 <170> SOFTWARE: PatentIn version 3.0
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C--> (handwritten marginal note at line 16)

w-OK (handwritten marginal note at line 52)

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122 Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Pro Ile
123             35                  40                  45
125 gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg   192
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130 Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile
131 65                  70                  75                  80
133 gag gtc tgg aag ctc tac ttc act cac ccc cag gac gtt ccc gca atc   288
134 Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
135                     85                  90                  95
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RAW SEQUENCE LISTING   DATE: 02/14/2001
PATENT APPLICATION: US/09/269,860   TIME: 16:03:08

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146 Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr
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149 ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata     480
150 Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile
151 145                 150                 155                 160
153 agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc     528
154 Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile
155                 165                 170                 175
157 gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag     576
158 Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys
159             180                 185                 190
161 cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata atc     624
162 Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Ile
163         195                 200                 205
165 tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag     672
166 Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu
167     210                 215                 220
169 aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gaa ccg aaa     720
170 Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys
171 225                 230                 235                 240
173 atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att     768
174 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile
175                 245                 250                 255
177 cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act     816
178 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
179             260                 265                 270
181 tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag     864
182 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu
183         275                 280                 285
185 aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga     912
186 Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly
187     290                 295                 300
189 tta gaa agg gtg gcc cgc tac tcg atg gag gac gcg aag gta acc tat     960
190 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
191 305                 310                 315                 320
193 gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc    1008
194 Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
195                 325                 330                 335
197 gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc    1056
198 Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
199             340                 345                 350
201 gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca    1104
202 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
203         355                 360                 365
205 cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac    1152
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210 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile
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213 gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat    1248
214 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
215             405             410             415
217 aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac    1296
218 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Glu Glu Tyr Asp
219             420             425             430
221 gtg gct cct cag gta ggc cat aag ttc tgc aag gac ttc ccc ggc ttc    1344
222 Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
223             435             440             445
225 atc cca agc ctc ctc gga gac ctc ttg gag gag aga cag aag gta aag    1392
226 Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Val Lys
227     450             455             460
229 aag aag atg aag gcc act ata gac cca atc gag aag aaa ctc ctc gat    1440
230 Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Lys Lys Leu Leu Asp
231 465             470             475             480
233 tac agg caa cga gca atc aaa atc ctt gct aat agc ttc tac ggt tac    1488
234 Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly Tyr
235             485             490             495
237 tac ggc tat aca aag gcc cgc tgg tac tac aag gag tgc gcc gag agc    1536
238 Tyr Gly Tyr Thr Lys Ala Arg Trp Tyr Tyr Lys Glu Cys Ala Glu Ser
239             500             505             510
241 gtt acc ggt tgg ggc agg gag tac atc gag acc acg ata agg gaa ata    1584
242 Val Thr Gly Trp Gly Arg Glu Tyr Ile Glu Thr Thr Ile Arg Glu Ile
243             515             520             525
245 gag gag aaa ttt ggc ttt aaa gtc ctc tac gcg gac aca gat gga ttt    1632
246 Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Phe
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249 ttc gca aca ata cct gga gcg gac gcc gaa acc gtc aaa aag aag gca    1680
250 Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
251 545             550             555             560
253 aag gag ttc ctg gac tac atc aac gcc aaa ctg ccc ggc ctg ctc gaa    1728
254 Lys Glu Phe Leu Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu Glu
255             565             570             575
257 ctc gaa tac gag ggc ttc tac aag cgc ggc ttc ttc gtg acg aag aag    1776
258 Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys
259             580             585             590
261 aag tac gcg gtt ata gac gag gag gac aag ata acg acg cgc ggg ctt    1824
262 Lys Tyr Ala Val Ile Asp Glu Glu Asp Lys Ile Thr Thr Arg Gly Leu
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265 gaa ata gtt agg cgt gac tgg agc gag ata gcg aag gag acg cag gcg    1872
266 Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
267     610             615             620
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278 Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp
279                   660                 665                 670
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282 Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala
283         675                 680                 685
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287     690                 695                 700
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290 Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
291 705                   710                 715                 720
293 gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag        2208
294 Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln
295                   725                 730                 735
297 gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa        2256
298 Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
299                   740                 745                 750
301 gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg        2304
302 Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
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326         35                  40                  45
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330     50                  55                  60
333 Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile
334 65              70                  75                  80
337 Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
338             85                  90                  95
341 Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr
342             100                 105                 110
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346         115                 120                 125
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